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Brief Communication

# Multiplex ligation-dependent probe amplification (MLPA) analysis is an effective tool for the detection of novel intragenic *PLA2G6* mutations: Implications for molecular diagnosis

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ABSTRACT

Phospholipase associated neurodegeneration (PLAN) comprises a heterogeneous group of autosomal recessive neurological disorders caused by mutations in the *PLA2G6* gene. Direct gene sequencing detects ~85% mutations in infantile neuroaxonal dystrophy. We report the novel use of multiplex ligation-dependent probe amplification (MLPA) analysis to detect novel *PLA2G6* duplications and deletions. The identification of such copy number variants (CNVs) expands the PLAN mutation spectrum and may account for up to 12.5% of *PLA2G6* mutations. MLPA should thus be employed to detect CNVs of *PLA2G6* in patients who show clinical features of PLAN but in whom both disease-causing mutations cannot be identified on routine sequencing.



## Introduction

Autosomal recessive neurodegeneration associated with genetic defects in the *PLA2G6* gene [1] may present with a number of phenotypes [2] including presentation in infancy [3,4] (infantile neuroaxonal dystrophy, INAD, MIM256600), childhood (atypical neuroaxonal dystrophy, neurodegeneration with brain iron accumulation, NBIA MIM610217, Karak syndrome MIM608395) [4,5] and also in adulthood [6,7] (early-onset dystonia-parkinsonism MIM612953). Mutation detection rate is particularly high (80–90%) in children with classical clinical and radiological features of infantile PLAN [2,8].[1]

Classical INAD (infantile onset PLAN) accounts for the majority of cases, and is characterised by infantile onset truncal hypotonia and progressive psychomotor regression [3,4]. Over time, children develop bulbar dysfunction, pyramidal tract signs, optic atrophy, cerebellar features and extrapyramidal features [3,4,9–12]. MRI features can aid diagnosis [13–15]. The majority of patients have features of cerebellar atrophy [4]. Cerebellar gliosis is seen in the majority [4] but not all patients have this feature [16]. Some also have evidence of brain iron accumulation [3,4]. Generalised seizures are often reported [17–19]. Dysmorphia is rarely described [20]. Death usually occurs around the first decade [3,4].

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[1] *Abbreviations used:* PLAN, phospholipase associated neurodegeneration; MLPA, multiplex ligation-dependent probe amplification; ARMD, Alu recombination-mediated deletion.

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Not all patients with typical clinical features of infantile PLAN have mutations in the *PLA2G6* gene [4]. Possible explanations for this include genetic heterogeneity [1], *PLA2G6* defects within intronic sequence or regulatory regions and CNVs that are undetected by standard diagnostic mutational screening strategies [21]. In recent years, MLPA has emerged as a high resolution technique to determine relative DNA sequence dosage [22,23].

We describe four children with infantile PLAN referred for diagnostic *PLA2G6* screening in which both disease-causing mutations were not identified on direct gene sequencing. Further investigation with MLPA analysis detected a novel heterozygous duplication in patient 1 and a novel homozygous deletion in patients 2–4.

## Subjects and methods

### *Patients*

The patients described were referred to the West Midlands Regional Genetic Service for *PLA2G6* analysis by their local paediatric neurologist/geneticist. The medical case notes were analysed to delineate the clinical features on history and examination. MRI brain scans for patient 1 were reviewed independently by 2 paediatric neuroradiologists (with consensus agreement on disparities).

### *Molecular genetic investigation*

Techniques for DNA/RNA extraction, *PLA2G6* sequencing, MLPA analysis and molecular characterisation of the CNVs are outlined in Supplementary data 1.

## Results

### *Clinical cases*

#### *Patient 1*

Patient 1 was the first child of non-consanguineous healthy Caucasian parents. Early neurodevelopmental milestones were achieved. At 15 months, he developed gait instability and an alternating strabismus. Psychomotor regression ensued and by 19–20 months of age, there was loss of ambulation. Between 2 and 3 years he developed 4-limb spasticity. Speech regression was also evident. He developed severe bulbar dysfunction with excessive drooling and feeding difficulties requiring PEG feeding. Dystonia of all 4-limbs was also evident by age 5 years. He did not have any seizures.

On clinical examination (age 5 years) he was not dysmorphic or microcephalic, but had evidence of a right-sided manifest squint and bilateral horizontal nystagmus. There was excessive drooling and tongue fasciculation. On neurological assessment he was found to have marked axial hypotonia. There was a postural kyphotic curvature of the spine. Limb examination revealed symmetrical 4-limb hypertonicity and hyperreflexia but no contractures. Plantar reflexes were upgoing bilaterally.

MRI brain examination was undertaken at age 2 and 2.9 years (Fig. 1). Initial MRI scan showed evidence of a hypoplastic cerebellum and vermis (Fig. 1A and B). There was no evidence of optic nerve hypoplasia or white matter abnormalities. On repeat MR neuroimaging at age 2.9 years, there was progressive cerebellar atrophy (Fig. 1C and D). Although minimal basal ganglia abnormalities were noted on initial imaging (Fig. 1E), mild iron accumulation within the basal ganglia was evident on repeat imaging (Fig. 1F). Electromyographic (EMG) signs of chronic denervation were evident in the upper limbs, lower limbs and bulbar musculature. Nerve conduction studies were normal. On EEG, widespread high amplitude fast activity at 16–22 Hz was seen. Visual evoked potentials (VEP) and electroretinogram (ERG) was normal at age 2 years. Ophthalmological review detected bilateral temporal disc pallor. Histological examination of nerve tissue from a rectal biopsy (age 2 years) was normal.

#### *Patient 2*

Patient 2, a 4 year old girl was born to healthy consanguineous (2nd cousin) Irish parents. All early developmental milestones were appropriately achieved. Symptom onset at 9–10 months of age commenced with psychomotor regression. She stopped vocalising, developed complete loss of ambulation and could only sit for brief periods with extensive support. There was no evidence of seizures.

On clinical examination, at age 21 months, she was not dysmorphic or microcephalic. There was evidence of marked axial hypotonia and upper and lower limb spasticity (but no contractures or spinal deformity). She had evidence of nystagmus on clinical examination. Ophthalmological examination did not detect any abnormalities.

MRI brain (age 18 months) revealed cerebellar atrophy and a marginally narrow pons but no evidence of basal ganglia abnormalities. Electromyogram abnormalities were similar to patient 1. She did not have any other electrophysiological investigations (VER, ERG, EEG) or a sural/skin biopsy as repeated non-attendance at clinic appointments precluded further neurological investigation.

#### *Patients 3 and 4*

Patients 3 and 4, dizygotic male twins were born to healthy consanguineous (1st cousin) parents, of Irish origin. There was no family history of neurological disorders and the family were not known to be related to patient 2's kindred. The twins were born at 33 weeks gestation, but despite their prematurity, the postnatal course was uneventful. Early developmental milestones were appropriately achieved, but concerns were raised at 11 months of age as both children were yet to sit independently. At this stage both children were noted to have strabismus. Psychomotor regression ensued in both children with a gradual but progressive loss of cognitive and motor skills. A rapid decline in motor function was seen in patient 3 subsequent to a febrile viral illness at age 22 months. Following this illness, he developed infantile spasms associated with a hypsarrhythmic EEG pattern. At age 26 months, patient 4 also developed seizures (generalised tonic clonic episodes) with an EEG pattern of high voltage slow background with sharp and slow wave discharges seen independently in each temporal region. Repeat EEG (5 months later) showed mild excess of moderate voltage irregular slow activity with runs of high amplitude irregular delta activity with ill defined sharp components independently over both temporal regions. Both children had ophthalmological assessments showing optic atrophy. Over time, both children developed profound axial hypotonia, pyramidal tract features and bulbar dysfunction.

MRI brain (at 24 months of age in both children) revealed moderate cerebellar atrophy, but no cerebellar gliosis or brain iron accumulation. Electrophysiological investigation revealed absent sensory nerve action potentials associated with a myopathic pattern on EMG. No clear binocular pattern of vision was evident on VEP. A sural/skin biopsy was not undertaken in either patient.

### *Molecular genetic investigation*

#### *Direct sequencing of PLA2G6*

*Patient 1:* A heterozygous mutation (c.1674delG; p.Leu560TrpfsX5) was detected in exon 12 (Supplementary Fig. 1). A 2nd mutation was not detected.

*Patient 2–4:* Molecular analysis did not detect any mutations in exons 1–4 and 7–17 of the *PLA2G6* gene. Repeated failed attempts

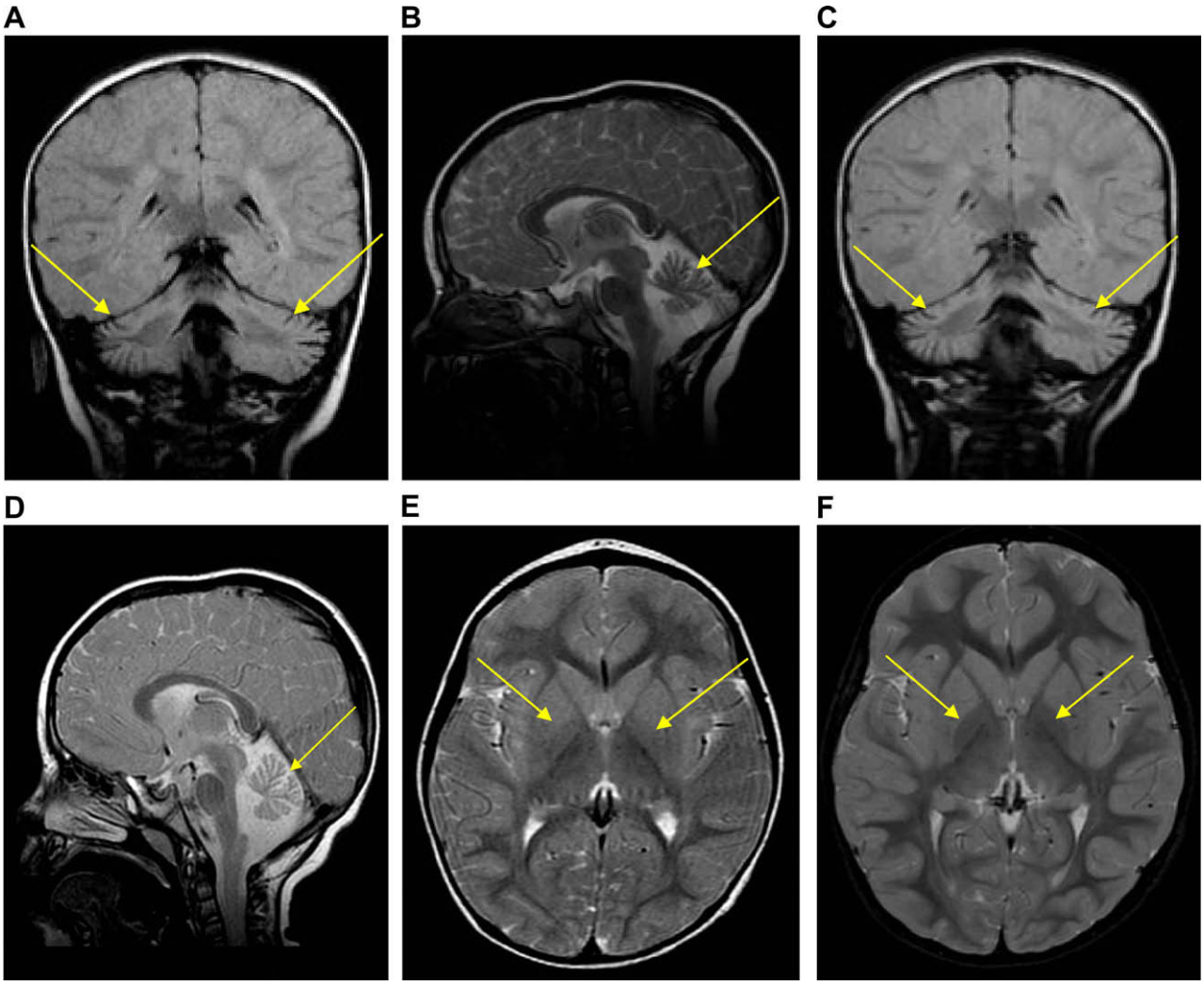


**Fig. 1.** MRI brain scan of patient 1. (A) and (B) Patient 1, age 2 years. (C) and (D) Patient 1, age 2.9 years. MR imaging. (E) Patient 1, age 2.0 years and (F) patient 1, age 2.9 years. (A) Coronal FLAIR sequence showing cerebellar atrophy, but no cerebellar grey matter gliosis. (B) Sagittal T2-weighted imaging showing marked atrophy of the cerebellar vermis. (C) Coronal FLAIR sequence shows cerebellar atrophy which is slightly worse than shown on previous scan at age 2 years (1A). Still no gliosis/abnormal signal is evident in the cerebellar grey matter. (D) Sagittal T2-weighted imaging showing marked atrophy of the cerebellar vermis. (E) Axial T2-weighted image showing very subtle decrease in T2 signal (compared to normal age-matched controls) in the globus pallidi. (F) Axial T2-weighted image showing further reduction in T2 signal within the globus pallidi.

to amplify exons 5 and 6 (due to polymerase chain reaction failure, Supplementary Fig. 2) raised the possibility of an intragenic homozygous deletion.

*MLPA analysis*

*Patient 1:* A heterozygous duplication of exons 4, 5, 6 and 7 was identified (Supplementary Fig. 3).

*Patient 2–4:* A homozygous deletion of exons 5 and 6 was detected in all patients (Supplementary Fig. 4).

*Molecular genetic characterisation of the CNVs*

*Patient 1:* Fig. 2A–D. Primers were designed for cDNA amplification of a putative tandem duplication from exon 7 to exon 4. Subsequent sequencing of patient 1 confirmed that the exon 4, 5, 6 and 7 duplication occurred within the *PLA2G6* gene leading to a pathogenic truncating mutation (r.426-?_1077-?dup p.Lys360LeufsX22).

*Patient 2–4:* Fig. 2E–G. PCR primers were designed to amplify the region between intron 4 and intron 6. The PCR amplification products were observed for patients but not in control samples. The genomic breakpoints were identified (g.40638_47282del6632, p.Leu204_Glu298del95) in intron 4 (between 38 537 112 and 38 537 123 bp) and in intron 6 (between 38 530 480 and 38 530 491 bp). The breakpoints could not be further delineated as there is a 12 bp region with 100% homology common to both intron 4 and intron 6.

## Discussion

To date, ~75 different genetic alterations of *PLA2G6* have been reported in PLAN [1–4,6,8,12,17] including missense mutations (~68%), insertions (~0.75%), deletions (~14%), nonsense mutations (~14%) and splice site mutations (~0.75%). We report the use of MLPA in the detection of previously undetected novel large intragenic *PLA2G6* rearrangements in four patients with classical infantile PLAN. Although this only a recently reported diagnostic use of MLPA in *PLA2G6* analysis [21], this diagnostic tool has already been successfully used in a number of other conditions [22,23] Indeed, MLPA analysis of the SCN1A gene in mutation-negative patients with Dravet's syndrome detected a significant chromosomal rear-

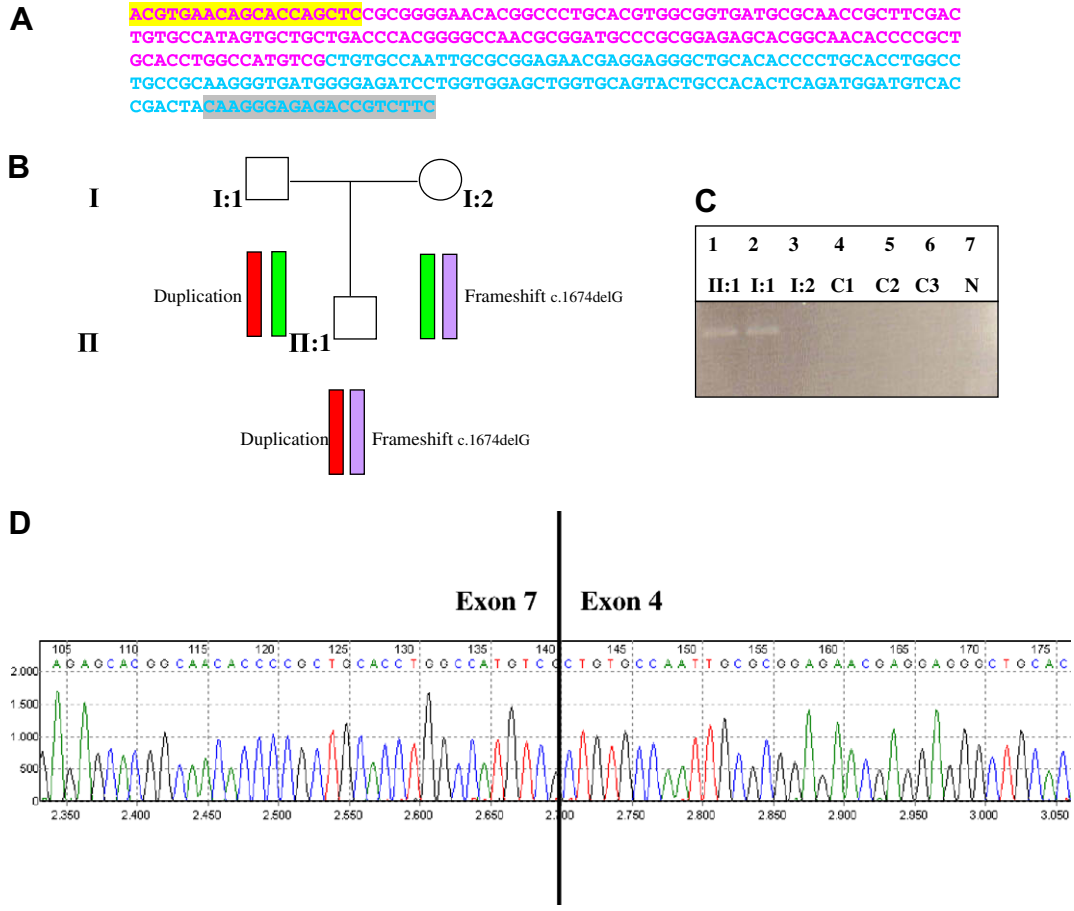


**Fig. 2.** Molecular genetic investigation of patient 1–4. (A)–(D) RNA analysis for patient 1. (E)–(G) Determination of the genomic deletion breakpoint in patients 2–4. (A) Forward and reverse primers designed to amplify a putative exon 7–4 junction fragment of 297 bp. Exon 7 sequence is highlighted in pink. Exon 4 sequence is highlighted in blue. Designed primers are highlighted in yellow (7F, forward primer) and grey (4R, reverse primer). (B) Pedigree of family 1 illustrating both parental and patient 1's disease alleles. (C) Agarose gel photograph of results of PCR amplification studies using primers 7F and 4R. Lane 1 – II:1 – Patient 1 – PCR product present. Lane 2 – I:1 – Father – PCR product present. Lane 3 – I:2 – Mother – PCR product absent. Lane 4 – C1 – Control sample – PCR product absent. Lane 5 – C2 – Control sample – PCR product absent. Lane 6 – C3 – Control sample – PCR product absent. Lane 7 – N – Negative control – PCR product absent. (D) Sequencing of PCR product in patient 1 (II:1) indicating that on RNA analysis, exon 7 is spliced to exon 4. (E) DNA sequence of the region in which the breakpoint occurs. Alu Y sequence shown in green, region of 100% homology highlighted grey. Intron 4 is in orange and intron 6 is in blue. Primers binding sites are underlined. (F) Agarose gel photograph of PCR amplification of introns 4 and 6 of the *PLA2G6* gene showing the presence of bands in patient 2 and their parents and the absence of bands in the normal control. Lane 1 – Normal control – No PCR product. Lane 2 – Patient 2 – PCR product of ~450 bp. Lane 3 – Patient 2's mother – PCR product of ~450 bp. Lane 4 – Patient 2's father – PCR product of ~450 bp. Lane 5 – 1 Kb ladder. (G) Schematic representation of the deletion breakpoint in patient 2. The exons that are present are indicated in red (exon 4 and 7). The deleted exons are represented in grey (exon 5 and 6). The black triangles represent the AluY repeats in introns 4 and 6. There is a 12 base region of homologous sequence which show 100% homology in both intron 4 and 6 (shaded yellow box). (For interpretation of the references in colour in this figure legend, the reader is referred to the web version of this article.)

rangement rate of 12.5% [24,25]. From this study, we estimate that CNVs may also account for ~12.5% *PLA2G6* mutations identified in the UK Diagnostic Screening Service.

MLPA analysis has important diagnostic implications. In patient 1, the heterozygous duplication could not be detected by standard direct gene sequencing. In patient 2, failed attempts to amplify exons 5 and 6 could have been due to a number of reasons (failed PCR amplification or the presence of rare SNP variants in primer binding regions). However MLPA alone cannot provide an insight as to the precise genomic location and/or potential functional outcomes of the deletion/duplication [26]. Subsequent molecular characterisation has provided important information regarding the nature of these CNVs. In case 1, analysis of cDNA revealed expression of mutant mRNA species containing a tandem duplication of exon 4, 5, 6, and 7, resulting in a frameshift and premature stop codon. In case 2, genomic delineation of the centromeric and telomeric breakpoints revealed that both breakpoints were within an AluY repeat sequence (http://www.repeatmasker.org/) in intron 4 and intron 6 (showing 94% overall homology) (www.blast.ncbi.nlm.nih.gov). An Alu recombination-mediated deletion (ARMD) as a result of misalignment of the Alu Y repeats is thus the most likely mechanism for generating this deletion. Deletion of exons 5 and 6 is predicted to lead to an inframe deletion which results in partial loss of the seven ankyrin repeats of the *PLA2G6* protein. Ankyrin repeats mediate protein–protein interactions and loss or disruption of this motif would be predicted to have a deleterious effect on normal iPLA$_2$-VI function.

## Conclusion

In conclusion, we describe the first reported use of MLPA in *PLA2G6* analysis. Our data suggests that CNVs also have a role in the pathogenesis of PLAN. As part of a *PLA2G6* diagnostic screening service, MLPA may contribute towards providing a definitive diagnosis in an affected individual. It may also help remove the need for unnecessary neurological investigation, improve the quality of genetic counselling and aid accurate prenatal diagnoses. It can

**E**

ctcgtgccaccacatgggctaattttttttttttttgagacggagtcttgctctgtcgcccaggctggagtgcag
tggcgcgatcttggctcactgcaagctctgcctcccgggttcatgccatcctcctgcctcagcctccagagtagc
tgggactacaggcgcccgccaccacacccggctaatttttttgtatttttagtagagacagggtttcaccgtgtt
cgccaggatggtcttggtctcctgaccttgtgatccgcctgcctcggcctcccaaagtgctgggattacaggcgt
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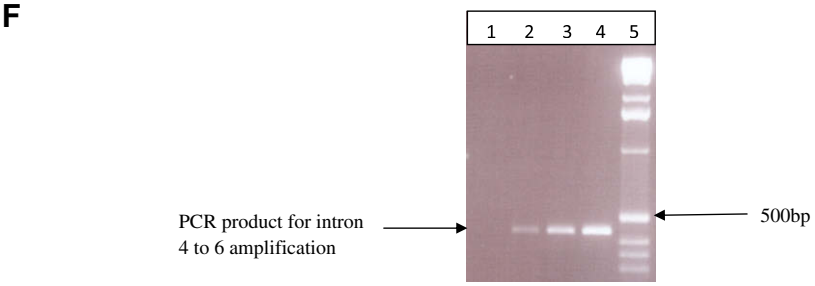
**F**




**G**

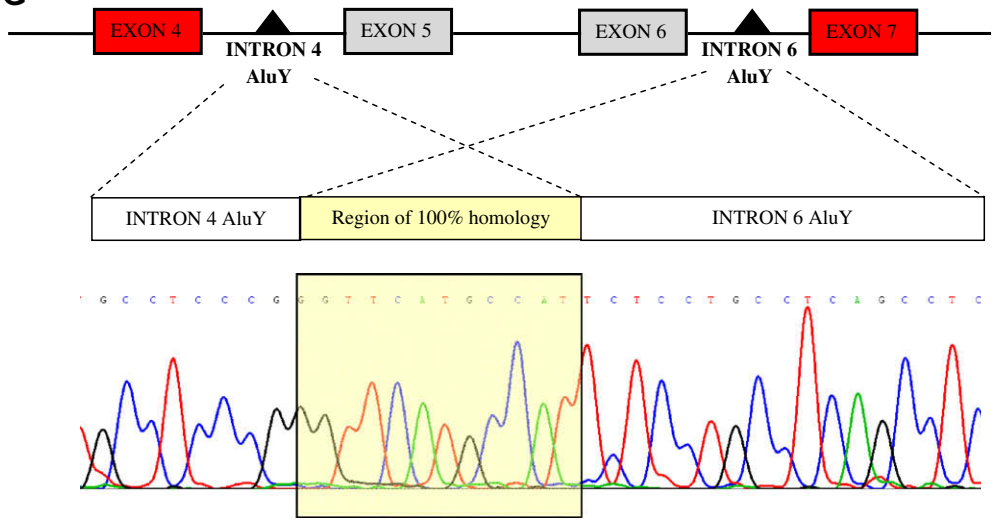



**Fig. 2** (*continued*)

provide greater understanding of disease genotype–phenotype correlation as well as insights into sequence-related chromosomal breakpoints, recombination hotspots and disease mechanisms. Our observations thus have implications for molecular diagnosis and highlight the importance of MLPA as a second-line diagnostic tool and adjunct to direct sequencing in *PLA2G6* screening.

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## Appendix A. Supplementary data

Supplementary data associated with this article can be found, in the online version, at doi:10.1016/j.ymgme.2010.02.009.

## References

[1] N.V. Morgan, S.K. Westaway, J.E. Morton, A. Gregory, P. Gissen, S. Sonek, H. Cangul, J. Coryell, N. Canham, N. Nardocci, G. Zorzi, S. Pasha, D. Rodriguez, I. Desguerre, A. Mubaidin, E. Bertini, R.C. Trembath, A. Simonati, C. Schanen, C.A. Johnson, B. Levinson, C.G. Woods, B. Wilmot, P. Kramer, J. Gitschier, E.R. Maher, S.J. Hayflick, PLA2G6, encoding a phospholipase A2, is mutated in neurodegenerative disorders with high brain iron, Nat. Genet. 38 (2006) 752–754.

[2] A. Gregory, B.J. Polster, S.J. Hayflick, Clinical and genetic delineation of neurodegeneration with brain iron accumulation, J. Med. Genet. 46 (2009) 73–80.

[3] M.A. Kurian, N.V. Morgan, L. MacPherson, K. Foster, D. Peake, R. Gupta, S.G. Philip, C. Hendriksz, J.E. Morton, H.M. Kingston, E.M. Rosser, E. Wassmer, P. Gissen, E.R. Maher, Phenotypic spectrum of neurodegeneration associated with mutations in the PLA2G6 gene (PLAN), Neurology 70 (2008) 1623–1629.

[4] S.K. Westaway, I.E. Holm, P.T. Kotzbauer, P. Hogarth, S. Sonek, J.C. Coryell, T.M. Nguyen, N. Nardocci, G. Zorzi, D. Rodriguez, I. Desguerre, E. Bertini, A. Simonati, B. Levinson, C. Dias, C. Barbot, I. Carrilho, M. Santos, I. Malik, J. Gitschier, S.J. Hayflick, Neurodegeneration associated with genetic defects in phospholipase A(2), Neurology 71 (2008) 1402–1409.

[5] A. Mubaidin, E. Roberts, D. Hampshire, M. Dehyyat, A. Shurbaji, M. Mubaidien, A. Jamil, A. Al-Din, A. Kurdi, C.G. Woods, Karak syndrome: a novel degenerative disorder of the basal ganglia and cerebellum, J. Med. Genet. 40 (2003) 543–546.

[6] C. Paisan-Ruiz, K.P. Bhatia, A. Li, D. Hernandez, M. Davis, N.W. Wood, J. Hardy, H. Houlden, A. Singleton, S.A. Schneider, Characterization of PLA2G6 as a locus for dystonia-parkinsonism, Ann. Neurol. 65 (2009) 19–23.

[7] F. Sina, S. Shojaee, E. Elahi, C. Paisán-Ruiz, R632W mutation in PLA2G6 segregates with dystonia-parkinsonism in a consanguineous Iranian family, Eur. J. Neurol. 16 (2009) 1–4.

[8] M.A. Kurian, D. Crompton, P. Rehal, N.V. Morgan, P. Gissen, F. Macdonald, E.R. Maher, Evaluation of the diagnostic screening service for *PLA2G6* mutations in phospholipase associated neurodegeneration (PLAN), Dev. Med. Child Neurol. 51 (2009) 16.

[9] J. Aicardi, P. Castelein, Infantile neuroaxonal dystrophy, Brain 102 (1979) 727–748.

[10] N. Nardocci, G. Zorzi, L. Farina, S. Binelli, W. Scaioli, C. Ciano, L. Verga, L. Angelini, M. Savoiardo, O. Bugiani, Infantile neuroaxonal dystrophy: clinical spectrum and diagnostic criteria, Neurology 52 (1999) 1472–1478.

[11] L. Farina, N. Nardocci, M.G. Bruzzone, L. D'Incerti, G. Zorzi, L. Verga, M. Morbin, M. Savoiardo, Infantile neuroaxonal dystrophy: neuroradiological studies in 11 patients, Neuroradiology 41 (1999) 376–380.
[12] I. Carrilho, M. Santos, A. Guimarães, J. Teixeira, R. Chorão, M. Martins, C. Dias, A. Gregory, S. Westaway, T. Nguyen, S. Hayflick, C. Barbot, Infantile neuroaxonal dystrophy: what's most important for the diagnosis?, Eur J. Paediatr. Neurol. 12 (2008) 491–500.
[13] L. Farina, N. Nardocci, M.G. Bruzzone, L. D'Incerti, G. Zorzi, L. Verga, M. Morbin, M. Savoiardo, Infantile neuroaxonal dystrophy: neuroradiological studies in 11 patients, Neuroradiology 41 (1999) 376–380.
[14] Y. Tanabe, M. Iai, M. Ishii, et al., The use of magnetic resonance imaging in diagnosing infantile neuroaxonal dystrophy, Neurology 43 (1993) 110–113.
[15] A. McNeill, D. Birchall, S.J. Hayflick, A. Gregory, J.F. Schenk, E.A. Zimmerman, H. Shang, H. Miyajima, P.F. Chinnery, T2* and FSE MRI distinguishes four subtypes of neurodegeneration with brain iron accumulation, Neurology 70 (2008) 1614–1619.
[16] R. Biancheri, A. Rossi, G. Alpigiani, M. Filocamo, C. Gandolfo, R. Lorini, C. Minetti, Cerebellar atrophy without cerebellar cortex hyperintensity in infantile neuroaxonal dystrophy (INAD) due to PLA2G6 mutation, Eur. J. Paediatr. Neurol. 11 (2007) 175–177.
[17] Y. Wu, Y. Jiang, Z. Gao, J. Wang, Y. Yuan, H. Xiong, X. Chang, X. Bao, Y. Zhang, J. Xiao, X. Wu, Clinical study and PLA2G6 mutation screening analysis in Chinese patients with infantile neuroaxonal dystrophy, Eur. J. Neurol. 16 (2009) 240–245.
[18] B.W. Scheithauer, L.S. Forno, L.J. Dorfman, C.A. Kane, Neuroaxonal dystrophy (Seitelberger's disease) with late onset, protracted course and myoclonic epilepsy, J. Neurol. Sci. 36 (1978) 247–258.
[19] F. Barontini, M. Papini, Late infantile neuroaxonal dystrophy. An unusual case with predominantly myoclonic-epileptic symptomatology, Riv. Patol. Nerv. Ment. 101 (1981) 171–184.
[20] M. Seven, A. Ozkilic, A. Yuksel, Dysmorphic face in two siblings with infantile neuroaxonal dystrophy, Genet. Couns. 13 (2002) 465–473.
[21] E.V. Haverfield, M.A. Dempsey, A. Gregory, S.K. Westaway, S.J. Hayflick, S. Das, Intragenic deletion and duplication analysis of the PANK2 and PLA2G6 genes in patients with NBIA, ACMG Annual Meeting, Phoenix, AZ, 2008.
[22] J.P. Schouten, C.J. McElgunn, R. Waaijer, D. Zwijnenburg, F. Diepvens, G. Pals, Relative quantification of 40 nucleic acid sequences by multiplex ligation-dependent probe amplification, Nucleic Acids Res. 30 (2002) e57.
[23] P. Kozlowski, A.J. Jasinska, D.J. Kwiatkowski, New applications and developments in the use of multiplex ligation-dependent probe amplification, Electrophoresis 29 (2008) 4627–4636.
[24] C. Depienne, O. Trouillard, C. Saint-Martin, I. Gourfinkel-An, D. Bouteiller, W. Carpentier, B. Keren, B. Abert, A. Gautier, S. Baulac, A. Arzimanoglou, C. Cazeneuve, R. Nabbout, E. LeGuern, Spectrum of SCN1A gene mutations associated with Dravet syndrome: analysis of 333 patients, J. Med. Genet. 46 (2009) 183–191.
[25] C. Marini, I.E. Scheffer, R. Nabbout, D. Mei, K. Cox, L.M. Dibbens, J.M. McMahon, X. Iona, R.S. Carpintero, M. Elia, M.R. Cilio, N. Specchio, L. Giordano, P. Striano, E. Gennaro, J.H. Cross, S. Kivity, M.Y. Neufeld, Z. Afawi, E. Andermann, D. Keene, O. Dulac, F. Zara, S.F. Berkovic, R. Guerrini, J.C. Mulley, SCN1A duplications and deletions detected in Dravet syndrome: implications for molecular diagnosis, Epilepsia 11 (2009) 1670–1678.
[26] A. McCart, A. Latchford, E. Volikos, A. Rowan, I. Tomlinson, A. Silver, A novel exon duplication event leading to a truncating germ-line mutation of the APC gene in a familial adenomatous polyposis family, Fam. Cancer 5 (2006) 205–208.